Figure S5: **Minimum genome length depends on phenotypic complexity.** To identify the minimal genome length, we reduced the genome size of all organisms with single-trait phenotypes a step-by-step fashion, removing one randomly chosen instruction at a time while preserving viability and phenotype. Single-trait phenotypes are arranged from left to right in order of increasing complexity (measured as the minimum number of times that a *nand* instruction must be executed to compute the logic function corresponding to that phenotype.